## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT:

Hall, Frederick L.

Gordon, Erlinda M.

Anderson, W. French

Starnes, Vaughn A.

(ii) TITLE OF INVENTION: Modified Retroviral Envelope

Polypeptides for Binding to

Extracellular Matrix

Components

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Carella, Byrne, Bain,

Gilfillan, Cecchi, Stewart &

Olstein

(B) STREET: 6 Becker Farm Road

(C) CITY: Roseland

(D) STATE: New Jersey

(E) COUNTRY: USA

(F) ZIP: 07068

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch diskette

(B) COMPUTER: IBM PS/2

(C) OPERATING SYSTEM: MS-DOS

(D) SOFTWARE: Word Perfect 5.1

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

## (B) FILING DATE:

- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Olstein, Elliot M.
  - (B) REGISTRATION NUMBER: 24,025
  - (C) REFERENCE/DOCKET NUMBER: 271010-364
- (ix) TELECOMMUNCIATION INFORMATION:
  - (A) TELEPHONE: 201-994-1700
  - (B) TELEFAX: 201-994-1744
- (2) INFORMATION FOR SEQ ID NO: 1:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 229 amino acids
    - (B) TYPE: amino acids
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: polypeptide
  - (ix) FRATURE:
    - (A) NAME/KEY: Receptor binding region of ecotropic gp70 protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Ser Pro Gly Ser Ser Pro

5

His Gln Val Tyr Asn Ile Thr Trp Glu Val

10 15

Thr Asn Gly Asp Arg Glu Thr Val Trp Ala

20 2!

Thr Ser Gly Asn His Pro Leu Trp Thr Trp

30 35

Trp Pro Asp Leu Thr Pro Asp Leu Cys Met

0 41

Leu Ala His His Gly Pro Ser Tyr Trp Gly

. 5

Leu Glu Tyr Gln Ser Pro Phe Ser Ser Pro

65 60 Pro Gly Pro Pro Cys Cys Ser Gly Gly Ser 75 70 Ser Pro Gly Cys Ser Arg Asp Cys Glu Glu Pro Leu Thr Ser Leu Thr Pro Arg Cys Asn 90 Thr Ala Trp Asn Arg Leu Lys Leu Asp Gln Thr Thr His Lys Ser Asn Glu Gly Phe Tyr 115 110 Val Cys Pro Gly Pro His Arg Pro Arg Glu 120 Ser Lys Ser Cys Gly Gly Pro Asp Ser Phe 135 130 Tyr Cys Ala Tyr Trp Gly Cys Glu Thr Thr 145 140 Gly Arg Ala Tyr Trp Lys Pro Ser Ser Ser 150 Trp Asp Phe Ile Thr Val Asn Asn Asn Leu 165 160 Thr Ser Asp Gln Ala Val Gln Val Cys Lys Asp Asn Lys Trp Cys Asn Pro Leu Val Ile 185 180 Arg Phe Thr Asp Ala Gly Arg Arg Val Thr 195 190 Ser Trp Thr Thr Gly His Tyr Trp Gly Leu 200 Arg Leu Tyr Val Ser Gly Gln Asp Pro Gly 210 Leu Thr Phe Gly Ile Arg Leu Arg Tyr Gln 225 220 Asn Leu

INFORMATION FOR SEQ ID NO: 2:

(2)

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 687 bases  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: polynucleotide  (ix) FEATURE:  (A) NAME/KEY: polynucleotide encoding receptor binding region of ecotropic gp70 protein  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  GCTTCGCCCG GCTCCAGTCC TCATCAAGTC TATAATATCA CCTGGGAGGT AACCAATGGA 60 GATCGGGAAGA CGGTATGGGC AACCTCCTC TGTGGACCTG GTGGCCTGAC 120
(A) LENGTH: 687 bases  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: polynucleotide  (ix) FEATURE:  (A) NAME/KEY: polynucleotide encoding receptor binding region of ecotropic gp70 protein  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
(B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: polynucleotide  (ix) FEATURE:  (A) NAME/KEY: polynucleotide encoding receptor binding region of ecotropic gp70 protein  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
(C) STRANDEDNESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: polynucleotide  (ix) FEATURE:  (A) NAME/KEY: polynucleotide encoding receptor binding region of ecotropic gp70 protein  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
(C) STRANDEDNESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: polynucleotide  (ix) FEATURE:  (A) NAME/KEY: polynucleotide encoding receptor binding region of ecotropic gp70 protein  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
(ii) MOLECULE TYPE: polynucleotide  (ix) FEATURE:  (A) NAME/KEY: polynucleotide encoding receptor binding region of ecotropic gp70 protein  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
(ix) FEATURE:  (A) NAME/KEY: polynucleotide encoding receptor binding region of ecotropic gp70 protein  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  GCTTCGCCCG GCTCCAGTCC TCATCAAGTC TATAATATCA CCTGGGAGGT AACCAATGGA 60
(A) NAME/KEY: polynucleotide encoding receptor binding region of ecotropic gp70 protein  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  GCTTCGCCCG GCTCCAGTCC TCATCAAGTC TATAATATCA CCTGGGAGGT AACCAATGGA 60
(A) NAME/KEY: polynucleotide encoding receptor binding region of ecotropic gp70 protein  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  GCTTCGCCCG GCTCCAGTCC TCATCAAGTC TATAATATCA CCTGGGAGGT AACCAATGGA 60
binding region of ecotropic gp70 protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  GCTTCGCCCG GCTCCAGTCC TCATCAAGTC TATAATATCA CCTGGGAGGT AACCAATGGA 60
protein  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  GCTTCGCCCG GCTCCAGTCC TCATCAAGTC TATAATATCA CCTGGGAGGT AACCAATGGA  60
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  GCTTCGCCCG GCTCCAGTCC TCATCAAGTC TATAATATCA CCTGGGAGGT AACCAATGGA 60
GCTTCGCCCG GCTCCAGTCC TCATCAAGTC TATAATATCA CCTGGGAGGT AACCAATGGA 60
GCTTCGCCCG GCTCCAGTCC TCATCAAGTC TATAATATCA CCTGGGAGGT AACCAATGGA 60  120
GCTTCGCCCG GCTCCAGTCC TCATCAAGTC TATAATATCA CCTGGGAGGT AACCTTGCCC AACCACCCTC TGTGGACCTG GTGGCCTGAC 120
GATCGGGAGA CGGTATGGGC AACTICIGGC AACTICIGGC AACTICIGGG CATAGAATAT 180
CTTACCCCAG ATTTATGTAT GTTAGCCCAC CATGGACCAT CTTATTGGGG GCTAGAATAT  CAATCCCCTT TTTCTTCTCC CCCGGGGCCC CCTTGTTGCT CAGGGGGCAG CAGCCCAGGC  240
TGTTCCAGAG ACTGCGAAGA ACCTTTAACC TCCCTCACCC CTCGGTGCAA CACTGCCTGG
TGTTCCAGAG ACTGCGAAGA ACCTTTAACC TCCCTCACCC CTCGGTGGTT GTTTGCCCC 360  AACAGACTCA AGCTAGACCA GACAACTCAT AAATCAAATG AGGGATTTTA TGTTTGCCCC 360
ARCAGACTCA AGCTAGACCA GACAACTCAT AAATCAAATC
TATTGGGGCT GTGAGACAAC CGGTAGAGCT TACTGGAAGC CCTCCTCATC ATGGGATTTC  480
ATCACAGTAA ACAACAATCT CACCTCTGAC CAGGCTGTCC AGGTATGCAA AGATAATAAG 540
ATCACAGTAA ACAACAATCI CACCICIGAC CAGGGTTAC TACCTGGACC  TGGTGCAACC CCTTAGTTAT TCGGTTTACA GACGCCGGGA GACGGGTTAC TTCCTGGACC  600
ACAGGACATT ACTGGGGCTT ACGTTTGTAT GTCTCCGGAC AAGATCCAGG GCTTACATTT 660
ACAGGACATT ACTGGGGCTT ACGTTTGTAT GTGTGGGGATCCGAC TCAGATACCA AAATCTA 687
GGGATCCGAC TCAGATACCA AAATCTA
(2) INFORMATION FOR SEQ ID NO: 3:
(i) SEQUENCE CHARACTERISTICS:
and
(A) LENGTH: 10 amino acid

į

- (2)
  - (B)
  - STRANDEDNESS: (C)
  - TOPOLOGY: linear (D)
  - (ii) MOLECULE TYPE: polypeptide
  - (ix) FRATURE:
    - NAME/KEY: collagen-binding of domain (A) von Willebrand Factor
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3: Trp Arg Glu Pro Ser Phe Met Ala Leu Ser

5